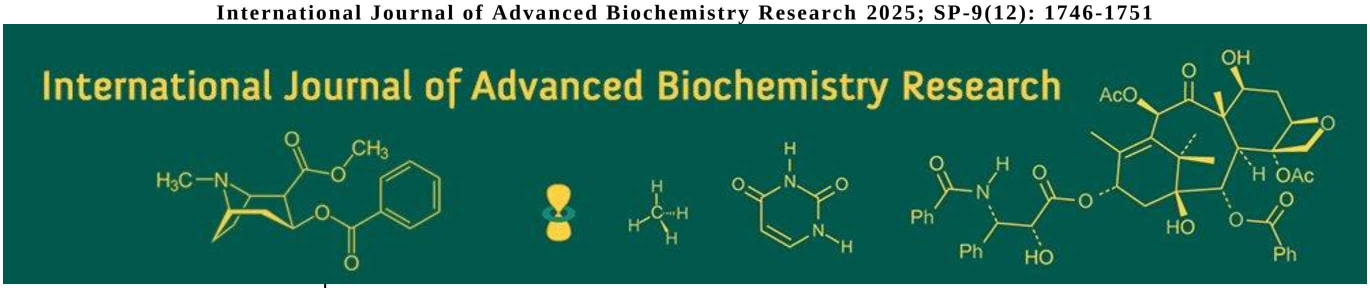
International Journal of Advanced Biochemistry Research 2025; SP-9(12): 1746-1751



International Journal of Advanced Biochemistry Research

Estimate of genetic variability and diversity in morphological traits of *Cassia tora* Linn

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DOI: https://www.doi.org/10.33545/26174693.2025.v9.i12Su.6810

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(12): 1746-1751
www.biochemjournal.com
Received: 09-10-2025
Accepted: 12-11-2025

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Abstract

The study aimed to investigate the genetic variability on the basis of genetical and morphological traits in *Cassia tora* Linn. The experiment was conducted during the *kharif* 2024 at the Research Cum Instructional Farm at Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh. Sixty-five accessions along with check were evaluated in a Randomized Complete Block Design with two replications. *Cassia tora* Linn is an important annual medicinal legume belonging to the family Leguminosae, widely distributed in tropical regions and valued for its galactomannan-rich seeds having therapeutic properties. Despite, its economic potential, systematic genetic improvement of this crop is limited. Therefore, the present study was undertaken to evaluate genetic variability, heritability, genetic advance, and genetic divergence for yield and its associated traits in *Cassia tora*. Observations were recorded on fifteen morphological and yield attributing traits for genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (broad sense), genetic advance and genetic diversity were estimated. The results indicated that PCV higher than GCV values, indicating influence of environmental for the expressions traits. The highest PCV and GCV was reported for number of pods per plant (43.76% and 99.70%), days to flowering (35.51% and 97.16%), number of tertiary branches per plant (36.15% and 95.37%), number of secondary branches per plant (35.99% and 95.92%), number of seeds per pod (24.33% and 81.64%) respectively. High heritability coupled with high genetic advance was observed in number of pod/plant (99.701 and 43.763) for these traits indicated the predominance of additive gene action, suggesting their suitability for direct selection. Cluster analysis showed highest inter-cluster distance between Cluster V (CG.CT-53) and Cluster VI (CG.CT-56), indicating their potential use as parents in hybridization programs for developing greater frequency of better segregants for developing new varieties.

Keywords: *Cassia tora Linn*, heritability, genetic advance, genetic variability, cluster analysis

Introduction

Cassia tora Linn, also known as sickle pod, wild senna or coffee pod, is an important annual leguminous plant. It is widely distributed across tropical regions of Asia and Africa and grows successfully in warm, moist soils, including uncultivated and wasteland areas. In India, particularly in Chhattisgarh, *Cassia tora* occurs naturally in districts such as Bastar, Bilaspur, Durg, and Surguja, where it plays a significant role in rural livelihoods and the medicinal plant economy Sonwani., *et al.* (2022).

Morphologically, *Cassia tora* is an annual herb with an erect and sturdy growth habit, attaining a height of about 30-90 cm. The main stem is upright, strong, and extensively branched, contributing to good canopy development. Leaves are compound, consisting of three pairs of opposite leaflets that are ovate to oblong in shape with an asymmetrical base. The leaf surface is smooth and green, supporting efficient photosynthesis. The plant bears bright yellow flowers with five petals, which emerge from the leaf axils. Flowering generally occurs during the rainy season, followed by fruiting in the winter season. The fruits are characteristic sickle-shaped pods, curved and elongated, measuring approximately 10-15 cm in length. Each pod contains about 30-50 seeds. The seeds are rhombohedral in shape, brown in color, and represent the most economically valuable part of the plant Sonwani., *et al.* (2022). This grows naturally in rural regions of Bastar, Bilaspur, Durg, and Surguja districts in Chhattisgarh.

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Among these, Surguja District contributes over 60% of the state's total Charota (*Cassia tora*) production. During the 2016 season, Jagdalpur District recorded a daily output of 300-350 quintals. According to Sonwani *et al.* (2018), the market price for *Cassia tora* seeds at that time ranged from ₹4,000 to ₹5,000 per quintal, or ₹40 to ₹60 per kilogram. For the collection year 2022-23, Ministry of tribal affairs announced the MSP for various minor forest produce items traded in Chhattisgarh. As per the marketing details presented, Charota (*Cassia tora*) is classified as an herb, and the seed is the economically important part. During 2022-23, the government procurement price of Charota seed was fixed at ₹1600 per quintal.The inclusion of Charota seed under the MSP framework provides price assurance and market support to forest-dependent communities, thereby contributing to income stability, livelihood security, and the strengthening of value chains for minor forest produce in the state.

From a quality perspective, *Cassia tora* seeds are a promising but underexploited source of galactomannan gum, which is structurally and chemically comparable to commercially important gums such as guar gum and locust bean gum valued for their dietary fibers and hydrocolloids. Cassia gum is known to form highly viscous aqueous dispersions when boiled in water and exhibits excellent thickening, stabilizing, and emulsifying properties. The plant has been traditionally used in indigenous and Chinese medicine systems for its laxative, diuretic, antiasthmatic, and vision-enhancing effects. It is as reported antioxidant, hypoglycemic, hypolipidemic, hepatoprotective, antimicrobial, antifungal, antihyperglycemic and antihypertensive activities associated with seed extracts. The water-soluble polysaccharides of *Cassia tora* have also been shown to bind bile acids and reduce cholesterol absorption, indicating their potential use as functional food ingredients.

Cassia tora as a crop with significant economic and industrial potential. Improvement in traits can be done only if the nature and amount of variability present in material is known. Few studies were done yet in Chhattisgarh in this context.

Materials and Methods

The field experiment was carried out at the Research Cum Instructional Farm of Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishawavidyalaya, Raipur, Chhattisgarh during the *kharif* 2024. The 65 *Cassia tora* accessions along with one checks viz. CGCT.M-22 were used as and experimental material planted in spacing 30 x 50cm in Randomized Complete Block Design with two replications. Recommended package of practices was followed to grow healthy crop. The germplasm was characterized as per the NBPGR descriptors. Five plants randomly selected from each accession and observation was recorded for fifteen traits viz. Days to flowering, Plant height (cm), No. of secondary branches per plant, No. of tertiary branches per plant, Internode length (cm), No. of pods per plant, Pod length (cm), Pod width (cm), 100 seed weight (g), Seed length (cm), Seed width (cm), Collar width (cm), No. of seed/pod, No. of seed/plant, Seed yield/plant (g).

Table 1: Experimental materials used in the study

S. No.	Accession No.	S. No.	Accession No.	S. No.	Accession No.
1	CG.CT-1	28	CG.CT-29	55	CG.CT-56
2	CG.CT-2	29	CG.CT-30	56	CG.CT-57
3	CG.CG-3	30	CG.CT-31	57	CG.CT-58
4	CG.CT-4	31	CG.CT-32	58	CG.CT-59
5	CG.CT-5	32	CG.CT-33	59	CG.CT-60
6	CG.CT-6	33	CG.CT-34	60	CG.CT-61
7	CG.CT-7	34	CG.CT-35	61	CG.CT-62
8	CG.CT-8	35	CG.CT-36	62	CG.CT-63
9	CG.CT-9	36	CG.CT-37	63	CG.CT-64
10	CG.CT-10	37	CG.CT-38	64	CG.CT-65
11	CG.CT-11	38	CG.CT-39	65	CG.CT-22 (C)
12	CG.CT-12	39	CG.CT-40		
13	CG.CT-13	40	CG.CT-41		
14	CG.CT-14	41	CG.CT-42		
15	CG.CT-15	42	CG.CT-43		
16	CG.CT-16	43	CG.CT-44		
17	CG.CT-17	44	CG.CT-45		
18	CG.CT-18	45	CG.CT-46		
19	CG.CT-19	46	CG.CT-47		
20	CG.CT-20	47	CG.CT-48		
21	CG.CT-21	48	CG.CT-49		
22	CG.CT-23	49	CG.CT-50		
23	CG.CT-24	50	CG.CT-51		
24	CG.CT-25	51	CG.CT-52		
25	CG.CT-26	52	CG.CT-53		
26	CG.CT-27	53	CG.CT-54		
27	CG.CT-28	54	CG.CT-55		

Results and Discussion

Analysis of variance for treatments were highly significant for all the traits, showed enough variability present among all the accessions studied Table.1.

Genotypic (GCV) and phenotypic (PCV) coefficients of variation are useful indicators to depict the variability within a population. The classification suggested by Sivasubramanium and Madhavamenon (1973) [8] categorizes these values as low (< 10%), moderate (10-20%), and high (> 20%). In present study PCV values was greater than GCV values, indicating the influence of the environment on the expression of trait. The high PCV and GCV percentage were recorded in Internode length (22.42%) and (33.57%) followed by number of pods per plant (21.27% and 21.30%) respectively. The number of tertiary branches per plant (17.96% and 18.39%), number of secondary branches per plant (17.84% and 18.21%), Days to flowering (17.49% and 17.74%), Plant height (16.98% and 17.04%), Seed width (12.79% and 16.75%), Seed length (12.38% and 15.73%) and number of seeds per plant (13.07% and 14.47%), all of these exhibited moderate levels of PCV and GCV respectively. This indicate the presence of considerable genetic variability.

Conversely, traits such as 100-seed weight (4.57% and 8.12%), number of seed per plant (6.30% and 8.09%), seed yield per plant (5.18% and 7.99%) and pod width (4.15% and 7.27%) showed low variability. These results are in accordance with the findings of Chandramohan *et al*. (2005) in *Cassia tora* and Mehra *et al.* (2020) in soybean.

Heritability reflects the proportion of phenotypic variation attributable to genetic factors, indicating the extent to which a trait can be passed from parents to progeny and is expressed as a percentage and it represents the genetic portion of the total observable variation in a population. Heritability estimates are generally classified into three categories: low when the value is below 50%, moderate when it ranges between 50-70%, and high when it is above 70%, as reported by Robinson (1966).

In the present investigation, most of the studied traits exhibited a high level of heritability. The high heritability was recorded for number of pods per plant (99.70%) followed by days to flowering (97.16%), number of secondary branches (95.92%), number of tertiary branches (95.37%), number of seeds per pod (81.64%) and seed length (61.96%). The result indicates a strong genetic control over these characteristics, suggesting that selection based on these traits would be highly effective. Similar finding was also reported by Sankarnarayanan (1994) in *Cassia* species. However, estimating heritability alone does not determine the potential genetic improvement achievable through selection of superior genotypes. Heritability values are considered meaningful only when they are accompanied by high genetic advance. To facilitate comparison of variability among different traits, genetic advance (GA) was evaluated as a percentage of the mean. Based on the magnitude of GA, traits were categorized into three classes: high (> 30%), moderate (10-30%), and low (<10%) as reported by Johnson *et al*. (1955).

The high genetic advance as a percentage of the mean was observed for the number of pods per plant (43.76%) followed by number of tertiary branches per plant (36.13%), number of secondary branches per plant (35.99%), days to flowering (35.51%), plant height (34.87%), internode length (30.86%) and number of seeds per plant (24.33%). Moderate GA% was recorded for number of seeds per plant (10.10%), seed length (20.08%) and seed width (20.11%).

High genetic advance coupled with high heritability was noted for number of pods per plant (43.76% and 99.70%), days to flowering (35.51% and 97.16%), number of tertiary branches per plant (36.13% and 95.37%), number of secondary branches per plant (35.99% and 95.92%) and number of seeds per pod (24.33% and 81.64%). This indicates the predominance of additive gene action in controlling these traits, suggesting that they can be effectively improved through selection. High heritability associated with moderate genetic advance as a percentage of mean was recorded for seed width (cm) and seed length (cm). The moderate to low GA% of the mean suggests the involvement of non-additive gene effects in the expression of trait Similar findings have also been reported by Chandramohanan *et al.* (2005) [2] and Abubakar *et al.* (2019) [1].

In present study quantitative assessment of genetic diversity was the studies using Mahalanobis's D^2 method on 65 accessions of *cassia tora*. The clustering of accession was dome in six groups present in Table.4. The maximum number of accession were found in Cluster I comprised the largest number of accession (45) followed by Cluster II with 11 accession and Cluster III with 4 accession. Clusters IV with 3 accession, Cluster V and VI each contained only a single accession.

Table 2: Analysis of variance for yield and yield attributing traits

S. No.	Source of Variation	Replication	Treatment	Error
1	Degree of freedom	1	64	64
2	Days to flowering	20.01	549.56**	7.91
3	Plant height (cm)	0.29	392.5**	1.32
4	No. of secondary branches /plant	0.65	19.30**	0.40
5	No. of tertiary branches /plant	0.28	33.61**	0.80
6	Internode length (cm)	0.91	5.00**	1.92
7	No. of pod/plant	0.09	533.13**	0.80
8	Pod length (cm)	11.04	5.67**	3.06
9	Pod width (cm)	0.04	0.01**	0.01
10	100-seed weight (g)	0.03	0.02**	0.02
11	Seed length (cm)	0.01	0.07**	0.00
12	Seed width (cm)	0.01	0.02**	0.00
13	Collar width (cm)	0.02	0.18**	0.10
14	No. of seed /pod	0.14	27.01**	2.73
15	No. of seed /plant	14,102.43	16514.6**	4,054.28
16	Seed yield/plant (g)	7.581	4.531**	1.844

** Significant at 1% Probability level

Table 3: Genetic parameters of variation for yield and its contributing traits

Genetic Parameters	Grand mean	Range		GCV (%)	PCV (%)	Heritability	GA% Mean
		Max	Min				
Days to flowering	94.085	115	63.5	17.491	17.745	97.161	35.517
Plant height (cm)	82.323	104	39.8	16.988	17.045	99.332	34.879
No. of secondary branches /plant	17.232	23.75	8.335	17.842	18.217	95.929	35.999
No. of tertiary branches /plant	22.554	40.5	9.75	17.961	18.392	95.371	36.133
Internode length (cm)	5.542	9.05	2.95	22.427	33.574	44.621	30.861
No. of pod/plant	76.681	100.835	32.915	21.276	21.308	99.701	43.763
Pod length (cm)	13.147	16.275	9.8	8.692	15.9	29.887	9.789
Pod width (cm)	1.518	1.7	1.325	4.157	7.274	32.663	4.894
100-seed weight (g)	1.838	2.005	1.405	4.547	8.122	31.339	5.243
Seed length (cm)	0.423	0.54	0.31	12.383	15.731	61.969	20.081
Seed width (cm)	0.237	0.325	0.2	12.792	16.758	58.269	20.115
Collar width (cm)	2.931	3.495	2.275	6.965	12.916	29.081	7.737
No. of seed /pod	26.649	40.495	21.375	13.076	14.471	81.644	24.339
No. seed /plant	1,252.86	1595	1052	6.3	8.094	60.579	10.101
Seed yield/plant (g)	22.343	26.11	20.025	5.188	7.991	42.155	6.939

Table 4: *Cassia tora*, clustering pattern of 65 accessions

Cluster group	Genotypes	Traits
Cluster I	45	CGCT13, CGCT14, CGCT15, CGCT16, CGCT17, CGCT18, CGCT19, CGCT20, CGCT21, CGCT22, CGCT25, CGCT26, CGCT27, CGCT28, CGCT30, CGCT31, CGCT32, CGCT33, CGCT35, CGCT36, CGCT37, CGCT38, CGCT39, CGCT40, CGCT41, CGCT42, CGCT43, CGCT44, CGCT45, CGCT46, CGCT47, CGCT48, CGCT49, CGCT50, CGCT51, CGCT52, CGCT54, CGCT55, CGCT57, CGCT58, CGCT59, CGCT60, CGCT61, CGCT62, CGCT8
Cluster II	11	CGCT 4, CGCT 5, CGCT10, CGCT11, CGCT34, CGCT6, CGCT63, CGCT64, CGCT65, CGCT7, CGCT9
Cluster III	4	CGCT12, CGCT23, CGCT24, CGCT29
Cluster IV	3	CGCT 1, CGCT 2, CGCT 3
Cluster V	1	CGCT53
Cluster VI	1	CGCT56

A higher level of genetic divergence among genotypes reflects greater distance between clusters. Genotypes showing greater divergence are valuable as they can produce a wide range of variability, providing enhanced opportunities for effective selection and crop improvement. For achieving maximum heterosis and generating broader genetic variation, parents should ideally be selected from clusters I and VI, as these clusters exhibit the largest inter-cluster distance.

Table 5: Average inter cluster mean values and intra cluster mean value for sixty-five genotypes for yield and yield attributing traits

Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	508.33	1856.45	1103.20	4717.14	1060.05	6523.25
Cluster II		471.16	4020.60	1177.94	2760.11	2265.51
Cluster III			480.65	7992.71	1269.84	10689.82
Cluster IV				174.10	5664.75	1057.71
Cluster V					0.00	8793.71
Cluster VI						0.00

The inter-cluster distances among the six clusters for yield and its related traits are presented in Table 5. The highest genetic distance was recorded between cluster III and cluster VI (10689.82) followed by Cluster V and Cluster VI (8793.71) Cluster III and Cluster IV (7992.71), and Cluster I and Cluster VI (6523.25). Conversely, the smallest intra-cluster distance was observed in Cluster IV (174.10), followed by Cluster II (471.16), Cluster III (480.65) and Cluster I (508.33).

The maximum inter-cluster distance noted between Cluster III and Cluster VI suggests that these groups contain the most genetically diverse genotypes. Since inter-cluster distances were consistently greater than intra-cluster distances, this confirms the presence of substantial genetic variability among the clusters. Thus, to create wider genetic variability in the segregating population, parents should be selected from genetically distant clusters for hybridization.

Table 6: Mean performance of genotypes in individual clusters for yield traits Cluster/Character

Trait	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
DFF	76	85.18	77.5	99.16	67.5	111.00
PH	57.77	67.74	101.54	86.72	84	39.80
SB	13.89	14.70	16	18.31	20.42	8.34
TB	21	19.07	25.13	23.17	40.50	9.75
IL	5.32	5.67	5.05	5.57	7.75	3.30

NP/PL	35.27	57.89	95.21	83.05	87.50	35.92
PL	13.39	13.11	12.42	13.22	15.38	10.10
PW	1.58	1.50	1.48	1.52	1.33	1.58
HSW	1.70	1.86	1.77	1.85	1.86	1.64
SL	0.39	0.38	0.40	0.43	0.51	0.48
SW	0.23	0.24	0.23	0.24	0.22	0.22
CW	28.02	28.77	25.24	25.95	39.78	23.25
NS/P	1304.17	1225.14	1307.38	1243.01	1294.50	1587.50
NS/PL	22.96	21.16	22.49	22.56	24.11	21.30
SY/PL	3.25	2.86	2.96	2.95	2.28	2.57

Note: DFF=Days to flowering, PH=Plant height, SB=Number of secondary branches/plant, TB=Number of tertiary branches/plant, IL=Internode length, NP/PL=Number of pod/plant, PL=Pod length, PW=Pod width, HSW=100 seed weight, SL=Seed length, SW=Seed width, CW=Collar width, NS/P=Number of seed/pod, NS/PL=Number of seed/plant, SY/PL=Seed yield/plant.

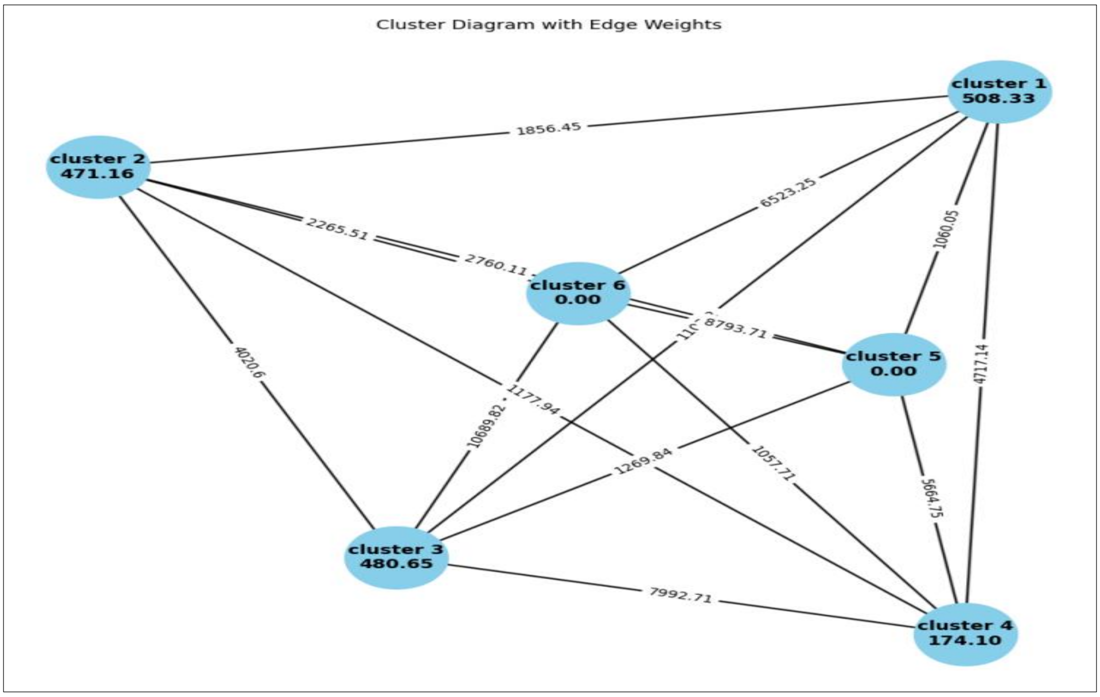

Fig 1: Cluster diagram with Intra and Inter cluster distances

Conclusion

The analysis of variance for treatment found was highly significant for all the traits under study indicating the presence of variation among the accession for all traits. The PCV showed high value then GVC depict influence of traits for expression of traits.

High PCV and GCV was ab observed in internode length (22.42% and 33.57%) followed by number of pods per plant (21.27% and 21.30%) respectively. High genetic advance coupled with high heritability for number of pods per plant, days to flowering, number of secondary and tertiary branches per plant, and number of seeds per pod indicates the predominance of additive gene action, suggesting that these traits can be effectively improved through direct selection. Traits such as seed length and seed width exhibited high heritability with moderate genetic advance, indicating the influence of non-additive gene effects. Therefore, priority should be given to traits with high heritability and genetic advance for achieving significant genetic improvement in yield.

Cluster analysis grouped the genotypes into six distinct and heterogeneous clusters, reflecting broad genetic diversity within the study material. Cluster I contained the highest number of genotypes, suggesting its wide genetic base, whereas Clusters V and VI were represented by single genotypes. The maximum inter-cluster divergence observed between Cluster III and Cluster VI (10689.82) suggests these groups as ideal candidates for hybridization. For the development of better segregates for developing new varieties.

Acknowledgement

The authors are thankful to the Department of Genetics and Plant Breeding and Plant Physiology, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, (C.G.) for its valuable support during entire research.

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